

# SEQUENCE LISTING

<110> Cahoon, Edgar B.  
Cahoon, Rebecca E.  
Kinney, Anthony J.  
Rafalski, J. Antoni

<120> TRIACYLGLYCEROL LIPASES

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<150> 60/083,688

<151> 1988-04-30

<150> PCT/US99/09280

<151> 1999-04-29

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<212> DNA

<213> Zea mays

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<213> Zea mays

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          20                      25                      30
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Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
          50                      55                      60
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Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser  
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Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu  
85 90 95

Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr  
100 105 110

Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys  
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35 40 45

Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys  
50 55 60

Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys  
65 70 75 80

Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile  
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35 40 45







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 20 25 30  
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 35 40 45  
 Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro  
 50 55 60  
 Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu  
 65 70 75 80  
 Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro  
 85 90 95  
 Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe  
 100 105 110  
 Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly  
 115 120 125  
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 145 150 155 160  
 Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr  
 165 170 175  
 Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr  
 180 185 190  
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 195 200 205  
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 210 215 220  
 Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu  
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 Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val  
 245 250 255  
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Arg Asn Thr Thr Asn Asp Ile Ser Asp Asp Lys Cys Pro Pro Gln Pro  
35 40 45  
His Pro Leu Xaa Met Cys Arg Ser Arg Val Ala Ala Tyr Gly Tyr Pro  
50 55 60  
Cys Glu Glu Tyr His Val Thr Thr Glu Asp Gly Tyr Ile Leu Ser Leu  
65 70 75 80  
Lys Lys Ile Pro Tyr Gly Leu Ser Gly Xaa Thr Xaa Ile Thr Arg Xaa  
85 90 95  
Pro Val Leu Leu Phe His Gly Leu Leu Val Asp Gly Phe Cys Trp Val  
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Gln Thr Gly Gln Lys Pro His Tyr Val Gly His Ser Met Gly Thr Leu  
35 40 45

Val Ala Leu Ala Ala Phe Ser Glu Gly Arg Val Val Ser Gln Leu Lys  
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 35 40 45  
 Gln Leu Leu Leu Pro Leu Gly Tyr Pro Cys Thr Glu His Asn Val Glu  
 50 55 60  
 Thr Lys Asp Gly Phe Leu Leu Ser Leu Gln His Ile Pro His Gly Lys  
 65 70 75 80  
 Asn Lys Ala Ala Asp Ser Thr Gly Pro Pro Val Phe Leu Gln His Gly  
 85 90 95



Leu	Phe	Gln	Gly 100	Gly	Asp	Thr	Trp	Phe 105	Ile	Asn	Ser	Ala	Glu 110	Gln	Ser
Leu	Gly	Tyr 115	Ile	Leu	Ala	Asp	Asn 120	Gly	Phe	Asp	Val	Trp 125	Ile	Gly	Asn
Val	Arg 130	Gly	Thr	Arg	Trp	Ser 135	Lys	Gly	His	Ser	Thr 140	Phe	Ser	Val	His
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Thr	Met	Pro 195	Glu	Ile	Val	Lys	Met 200	Ile	Ser	Ser	Ala	Ala 205	Leu	Leu	Cys
Pro	Ile 210	Ser	Tyr	Leu	Asp	His 215	Val	Ser	Ala	Ser	Phe 220	Val	Leu	Arg	Ala
Val 225	Ala	Met	His	Leu	Asp 230	Gln	Met	Leu	Val	Thr 235	Met	Gly	Ile	His	Gln 240
Leu	Asn	Phe	Arg	Ser 245	Asp	Met	Gly	Val	Gln 250	Ile	Val	Asp	Ser	Leu 255	Cys
Asp	Gly	Glu	His 260	Val	Asp	Cys	Asn	Asn 265	Leu	Leu	Ser	Ala	Ile 270	Thr	Gly
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Ile 305	Arg	Lys	Gly	Thr	Phe 310	Ala	Lys	Tyr	Asp	Tyr 315	Gly	Leu	Leu	Gly	Asn 320
Leu	Arg	Arg	Tyr	Gly 325	His	Leu	Arg	Pro	Pro 330	Ala	Phe	Asp	Leu	Ser 335	Ser
Ile	Pro	Glu	Ser 340	Leu	Pro	Ile	Trp	Met 345	Gly	Tyr	Gly	Gly	Leu 350	Asp	Ala
Leu	Ala	Asp 355	Val	Thr	Asp	Val	Gln 360	Arg	Thr	Ile	Arg	Glu 365	Leu	Gly	Ser
Thr	Pro 370	Glu	Leu	Leu	Tyr	Ile 375	Gly	Asp	Tyr	Gly	His 380	Ile	Asp	Phe	Val
Met 385	Ser	Val	Lys	Ala	Lys 390	Asp	Asp	Val	Tyr	Val 395	Asp	Leu	Ile	Arg	Phe 400
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His Leu Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr  
35 40 45  
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<212> DNA  
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gaatttaatc caaaagggtt agctgttgat gcctttctca agtctctctg tgtcaccct 960  
gggatagact gctatgactt gttgactgca ctaactggta aaaattgctg cctcaattct 1020  
tcaactgttg atctattctt gatgaatgag cctcagtcaa catcaacaaa gaacatggtg 1080  
cacttggtc agactgttag acttggggcg ttgacaaaat tcaattatgt gagaccagac 1140  
tataacatta tgcactatgg agaaatattt cctccaatct ataacctttc caacatcccc 1200  
cacgatctcc ctctcttcat tagctatggt ggaagagatg cactttcaga tgtccgtgat 1260  
gttgagaatt tgcttgataa actcaagttc catgatgaga acaagcgag cgttcagttc 1320  
atccaggaat atgctcatgc tgactacatt atgggggttca atgccaagga cttggtgat 1380  
aatgctgttc tttcattttt caatcatcaa gtttaacact ggatagaatg aatcaagttg 1440  
tatgaaaaga gtgccttcat gtattaggta gctatcattg agatcaatct aagttatcta 1500  
gtggagatta agtaacggct aattacaaaa gtaatgaagt attatcacta gtgatttgct 1560  
ttgggtgttc aaatggctat tgcactctat tattgtgttg cattgtaatg cagaggaaaag 1620  
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ttataaaaaac tatgtttcca aaaaaaaaaa aaaaaaaaaa 1718

<210> 18  
<211> 410  
<212> PRT  
<213> Glycine max

<400> 18  
Met Ala Leu Leu Gly Leu Met Ser Phe Ala Ala Leu Thr Leu Phe Leu  
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Val Leu Thr Thr Val Pro Arg Gln Ala His Ala Ser Ser Arg Gly Asn  
20 25 30  
Leu Gly Arg Asn Ile Asn Pro Ser Val Tyr Gly Ile Cys Ala Ser Ser  
35 40 45  
Val Ile Val His Gly Tyr Lys Cys Gln Glu His Glu Val Thr Thr Asp  
50 55 60  
Asp Gly Tyr Ile Leu Ser Leu Gln Arg Ile Pro Glu Gly Arg Gly Lys  
65 70 75 80  
Ser Ser Gly Ser Gly Thr Arg Lys Gln Pro Val Val Ile Gln His Gly  
85 90 95  
Val Leu Val Asp Gly Met Thr Trp Leu Leu Asn Pro Pro Glu Gln Asp  
100 105 110



Leu	Pro	Leu	Ile	Leu	Ala	Asp	Asn	Gly	Phe	Asp	Val	Trp	Ile	Ala	Asn
		115					120					125			
Thr	Arg	Gly	Thr	Arg	Tyr	Ser	Arg	Arg	His	Ile	Ser	Leu	Asp	Pro	Ser
	130					135					140				
Ser	Gln	Ala	Tyr	Trp	Asn	Trp	Ser	Trp	Asp	Glu	Leu	Val	Ser	Tyr	Asp
145					150					155					160
Phe	Pro	Ala	Val	Phe	Asn	Tyr	Val	Phe	Ser	Gln	Thr	Gly	Gln	Lys	Ile
				165					170					175	
Asn	Tyr	Val	Gly	His	Ser	Leu	Gly	Thr	Leu	Val	Ala	Leu	Ala	Ser	Phe
			180					185					190		
Ser	Glu	Gly	Lys	Leu	Val	Thr	Gln	Leu	Lys	Ser	Ala	Ala	Leu	Leu	Ser
		195					200					205			
Pro	Ile	Ala	Tyr	Leu	Ser	His	Met	Asn	Thr	Ala	Leu	Gly	Val	Val	Ala
	210					215					220				
Pro	Lys	Ser	Phe	Val	Gly	Glu	Ile	Thr	Thr	Leu	Phe	Gly	Leu	Ala	Glu
225					230					235					240
Phe	Asn	Pro	Lys	Gly	Leu	Ala	Val	Asp	Ala	Phe	Leu	Lys	Ser	Leu	Cys
				245					250					255	
Ala	His	Pro	Gly	Ile	Asp	Cys	Tyr	Asp	Leu	Leu	Thr	Ala	Leu	Thr	Gly
			260					265					270		
Lys	Asn	Cys	Cys	Leu	Asn	Ser	Ser	Thr	Val	Asp	Leu	Phe	Leu	Met	Asn
		275					280					285			
Glu	Pro	Gln	Ser	Thr	Ser	Thr	Lys	Asn	Met	Val	His	Leu	Ala	Gln	Thr
	290					295					300				
Val	Arg	Leu	Gly	Ala	Leu	Thr	Lys	Phe	Asn	Tyr	Val	Arg	Pro	Asp	Tyr
305					310					315					320
Asn	Ile	Met	His	Tyr	Gly	Glu	Ile	Phe	Pro	Pro	Ile	Tyr	Asn	Leu	Ser
				325					330					335	
Asn	Ile	Pro	His	Asp	Leu	Pro	Leu	Phe	Ile	Ser	Tyr	Gly	Gly	Arg	Asp
			340					345					350		
Ala	Leu	Ser	Asp	Val	Arg	Asp	Val	Glu	Asn	Leu	Leu	Asp	Lys	Leu	Lys
		355					360					365			
Phe	His	Asp	Glu	Asn	Lys	Arg	Ser	Val	Gln	Phe	Ile	Gln	Glu	Tyr	Ala
	370					375					380				
His	Ala	Asp	Tyr	Ile	Met	Gly	Phe	Asn	Ala	Lys	Asp	Leu	Val	Tyr	Asn
385					390					395					400
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				405					410						

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<210> 19
<211> 1438
<212> DNA
<213> Glycine max
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 145 150 155 160  
 Ile Asn Tyr Ile Asn Ser Val Thr Asn Ser Lys Ile Phe Val Val Gly  
 165 170 175  
 His Ser Gln Gly Thr Ile Ile Ser Leu Ala Ala Phe Thr Gln Pro Glu  
 180 185 190  
 Ile Val Glu Lys Val Glu Ala Ala Ala Leu Leu Ser Pro Ile Ser Tyr  
 195 200 205  
 Leu Asp His Val Ser Ala Pro Leu Val Leu Arg Met Val Lys Met His  
 210 215 220  
 Ile Asp Glu Met Ile Leu Thr Met Gly Ile His Gln Leu Asn Phe Lys  
 225 230 235 240  
 Ser Glu Trp Gly Ala Ser Leu Leu Val Ser Leu Cys Asp Thr Arg Leu  
 245 250 255  
 Ser Cys Asn Asp Met Leu Ser Ser Ile Thr Gly Lys Asn Cys Cys Phe  
 260 265 270  
 Asn Glu Ser Arg Val Glu Phe Tyr Leu Glu Gln Glu Pro His Pro Ser  
 275 280 285  
 Ser Ser Lys Asn Leu Asn His Leu Phe Gln Met Ile Arg Lys Gly Thr  
 290 295 300  
 Tyr Ser Lys Tyr Asp Tyr Gly Lys Leu Lys Asn Leu Ile Glu Tyr Gly  
 305 310 315 320  
 Lys Phe Asn Pro Pro Lys Phe Asp Leu Ser Arg Ile Pro Lys Ser Leu  
 325 330 335  
 Pro Leu Trp Met Ala Tyr Gly Gly Asn Asp Ala Leu Ala Asp Ile Thr  
 340 345 350  
 Asp Phe Gln His Thr Leu Lys Glu Leu Pro Ser Pro Pro Glu Val Val  
 355 360 365  
 Tyr Leu Glu Asn Tyr Gly His Val Asp Phe Ile Leu Ser Leu Gln Ala  
 370 375 380  
 Lys Gln Asp Leu Tyr Asp Pro Met Ile Ser Phe Phe Lys Ser Ser Gly  
 385 390 395 400  
 Lys Phe Ser Ser Met  
 405

<210> 21  
 <211> 737  
 <212> DNA  
 <213> Zea mays

<400> 21  
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 tcccaagaac aatccgtgtg acccatcaga atgatattgt gccgcattta ccaccgtatt 180  
 attattacct aggtgaatgg acataccacc acttcgctag agaggtttgg cttcatgaga 240



gcatagatgg aaatgtagtt accagaaaacg agacgggtatg tgatgattct ggtgaagacc 300  
cgacctgtag caggtcggtc tatgggatga gcgtagcaga tcatcttgag tactatgatg 360  
tcacactaca tgctgattca agaggaacct gtcaattcgt gattggtgca gccaaccaag 420  
tatacaacta cgttcgtgaa gttgatggat ccatcatcct gtcaagatac ccgcaagaac 480  
cacaagctct agaatctatg tgactttgta tgccacggaa tgcacccctg tacagtattt 540  
ttcattttca ttttgtgtac agctcatgaa atgctgggcg ctccctggagc tctccagagg 600  
ataaggagag gctcaccttt ttaaattgtgc cccctttgct caagtgagaa tcgtgcatgt 660  
aagctccata agattgtccg cacaattcaa tttgtgtata taaataatac tatgtgttac 720  
taaaaaaaaa aaaaaaa 737

<210> 22  
<211> 166  
<212> PRT  
<213> Zea mays

<400> 22  
Thr Arg Phe Cys Ala Leu Asp Leu Ser Val Lys Phe Gly Ser Gln Glu  
1 5 10 15  
Val Glu Leu Met Thr Phe Gly Gln Pro Arg Ile Gly Asn Pro Ala Phe  
20 25 30  
Ala Val Tyr Phe Gly Glu Gln Val Pro Arg Thr Ile Arg Val Thr His  
35 40 45  
Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Tyr Tyr Leu Gly  
50 55 60  
Glu Trp Thr Tyr His His Phe Ala Arg Glu Val Trp Leu His Glu Ser  
65 70 75 80  
Ile Asp Gly Asn Val Val Thr Arg Asn Glu Thr Val Cys Asp Asp Ser  
85 90 95  
Gly Glu Asp Pro Thr Cys Ser Arg Ser Val Tyr Gly Met Ser Val Ala  
100 105 110  
Asp His Leu Glu Tyr Tyr Asp Val Thr Leu His Ala Asp Ser Arg Gly  
115 120 125  
Thr Cys Gln Phe Val Ile Gly Ala Ala Asn Gln Val Tyr Asn Tyr Val  
130 135 140  
Arg Glu Val Asp Gly Ser Ile Ile Leu Ser Arg Tyr Pro Gln Glu Pro  
145 150 155 160  
Gln Ala Leu Glu Ser Met  
165

<210> 23  
<211> 1434  
<212> DNA  
<213> Zea mays

<220>  
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<222> (226)

<220>  
<221> unsure  
<222> (315)



[illegible]

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<222>   (1373)
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<220>	
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<220>	
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<400> 24

Leu Ser Ala Ala Ser His Gly Arg Glu Leu Pro Val Lys Ser Ser Asp  
20 25 30

Ala Xaa Ala Val Tyr Met Thr Asp Leu Thr Ala Leu Phe Thr Trp Thr  
50 55 60

Ile Val Asp Val Glu Lys Leu Leu Ala Gly Ile Val Gly Val Asp His  
85 90 95

Val Gln Asn Trp Ile Lys Asp Leu Ile Trp Lys Gln Leu Asp Leu Ser  
115 120 125

Tyr Asn Asn Thr Ile Leu Arg Leu Ala Ile Thr Ser Ala Val His Lys  
145 150 155 160

Met Gly Gly Ala Met Ala Ser Phe Cys Ala Leu Asp Leu Ala Met Lys  
180 185 190

Gly Asn Ala Ala Phe Ala Ser Tyr Phe Ala Lys Tyr Val Pro Asn Thr  
210 215 220

Phe Ser Phe Leu Pro Gln Leu Thr Tyr His His Phe Pro Arg Glu Val  
245 250 255

Ser Gly Glu Asp Pro Asp Cys Cys Arg Cys Ile Ser Met Phe Gly Leu  
275 280 285



<210> 25  
 <211> 1560  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (601)

<400> 25  
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 gcgctctccgc cgccgcggga tccggcgga tgactactac ttggacgtgg agagcggcag 180  
 gcggcgggtgc cgctggtgca gcagcagtag gtgaacgggc ggctcgtccg cctccgcacc 240  
 ttctccgtgt tcgaggtgag catgatggcc gccaaagatcg cctacgagaa cgccgcctac 300  
 atcgagaacg tcgtcaacaa cgtctggaag ttccacttcg tggggttcta caactgctgg 360  
 aacaagtctg tgggcgacca cagcagcgag gcggttcgtgt tcaccgacaa ggcaagagga 420  
 cgcgagcgtg gtggtggtgt cgttcggggg caccgagccc ttcaacatgc gggactggte 480  
 caccgacgta aacctgtcgt ggctgggcat gggcgagctg ggccacgtcc acgtcggctt 540  
 cctcaaggcg ctgggcctgc aggaggagga cggcaaggac gccacgcggg cgttcccca 600  
 nggcgcccc aacgcgctcc cgggcaagcc gctggcctac tacgcgctgc gcgaggaggt 660  
 ccagaagcag ctgcagaagc acccgaacgc caacgctcgt gtcaccggcc acagcctcgg 720  
 cgccgcgctg gcgacctct tcccggcgt gctggcgctt caccggggagc ggggcgtcct 780  
 ggaccgcctg ctctccgtgg tcacctacgg gcagccgcgc gtgggcgaca aggtgttcgc 840  
 gggctacgtg cgcgccaacg tgcccgtgga gccgctccgg gtggtgtacc gctacgacgt 900  
 ggtcccgcgc gtgccccttc acgcgcgcgc cgtcgccgac ttcgcgcacg gcggcacctg 960  
 cgtctacttc gacggctggt acaaggcccg cgagatcgcc aagggcggcg acgcgcccaa 1020  
 caagaactac ttcgaccca ggtacctgct gtccatgtac ggcaacgcgt ggggggacct 1080  
 cttcaaggcg gccttcctgt gggccaagga gggcaaggac taccgcgagg gcgcgctctc 1140  
 gctgctctac cgcgccaccg gcctgctcgt gcccggcatc gcgtcgaca gccccagga 1200  
 ctacgtcaac gccgtccgcc tcggcagcgt cgccctcgcg tagcttttgg attgcatgtt 1260  
 cgtttccatg catgtgtatc attgcatgca ataattggat gaaataaaca gcaataagct 1320  
 tcatcagtat tattattgtt gttgttgaat atatgcatcc tctcctctct atatagaatt 1380  
 atagatacat gaggcctggc cggccgcgca cgttgctgaa cagttgaagc gcttcccaaa 1440  
 aaaaaatgta tcaactgtga agcatatata tccatgcatg catgtgtgcc cgaaattttt 1500  
 gtttttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaacaaa aaaaaaaaaa 1560

<210> 26  
 <211> 258  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> UNSURE  
 <222> (45)

<400> 26  
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 1 5 10 15  
 Glu Leu Gly His Val His Val Gly Phe Leu Lys Ala Leu Gly Leu Gln  
 20 25 30  
 Glu Glu Asp Gly Lys Asp Ala Thr Arg Ala Phe Pro Xaa Gly Ala Pro  
 35 40 45  
 Asn Ala Val Pro Gly Lys Pro Leu Ala Tyr Tyr Ala Leu Arg Glu Glu  
 50 55 60



Val Gln Lys Gln Leu Gln Lys His Pro Asn Ala Asn Val Val Val Thr  
 65 70 75 80  
 Gly His Ser Leu Gly Ala Ala Leu Ala Thr Ile Phe Pro Ala Leu Leu  
 85 90 95  
 Ala Phe His Gly Glu Arg Gly Val Leu Asp Arg Leu Leu Ser Val Val  
 100 105 110  
 Thr Tyr Gly Gln Pro Arg Val Gly Asp Lys Val Phe Ala Gly Tyr Val  
 115 120 125  
 Arg Ala Asn Val Pro Val Glu Pro Leu Arg Val Val Tyr Arg Tyr Asp  
 130 135 140  
 Val Val Pro Arg Val Pro Phe Asp Ala Pro Pro Val Ala Asp Phe Ala  
 145 150 155 160  
 His Gly Gly Thr Cys Val Tyr Phe Asp Gly Trp Tyr Lys Gly Arg Glu  
 165 170 175  
 Ile Ala Lys Gly Gly Asp Ala Pro Asn Lys Asn Tyr Phe Asp Pro Arg  
 180 185 190  
 Tyr Leu Leu Ser Met Tyr Gly Asn Ala Trp Gly Asp Leu Phe Lys Gly  
 195 200 205  
 Ala Phe Leu Trp Ala Lys Glu Gly Lys Asp Tyr Arg Glu Gly Ala Val  
 210 215 220  
 Ser Leu Leu Tyr Arg Ala Thr Gly Leu Leu Val Pro Gly Ile Ala Ser  
 225 230 235 240  
 His Ser Pro Arg Asp Tyr Val Asn Ala Val Arg Leu Gly Ser Val Ala  
 245 250 255

Ser Ala

<210> 27  
 <211> 432  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> unsure  
 <222> (7)

<220>  
 <221> unsure  
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<220>  
 <221> unsure  
 <222> (27)

<220>  
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 <222> (38)



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<220>
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<222>  (50)
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<221>  unsure
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<221>  unsure
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<220>
<221>   unsure
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<221>  unsure
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<221>   unsure
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<400> 27						
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aggaagacat	atggaaggct	acctataaat	gtntaggnt	cantncgatg	ggagggnctt	120
tttagcatcg	ttcttgtgcc	cttgacctct	cttgttaagt	atggatcgca	ggaagtcaa	180
ctcatgactt	ttggacagcc	tcgggtaggc	aatccttctt	ttgctgcgta	cttcagtgc	240
caagtcocga	gaacaatccg	tgtgacctat	cagaatgaca	ttgtcccaca	cttgccacca	300
tatttttgtc	accttggcga	atggacatat	caccacttct	cgagagaggt	ttggcttcat	360
gagaccatag	taggaaatgt	agttactagg	aatgagacca	tctgtgatgg	atcaggcgag	420
gacccaacat	gc					432

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<210> 28
<211> 106
<212> PRT
<213> Oryza sativa
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<400> 28  
Gly Pro Phe Ser Ile Val Leu Val Pro Leu Thr Ser Leu Val Lys Tyr  
1 5 10 15

Gly Ser Gln Glu Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val Gly  
20 25 30

Asn Pro Ser Phe Ala Ala Tyr Phe Ser Asp Gln Val Pro Arg Thr Ile  
35 40 45

Arg Val Thr His Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Phe  
50 55 60

Cys Tyr Leu Gly Glu Trp Thr Tyr His His Phe Ser Arg Glu Val Trp  
65 70 75 80

Leu His Glu Thr Ile Val Gly Asn Val Val Thr Arg Asn Glu Thr Ile  
85 90 95

Cys Asp Gly Ser Gly Glu Asp Pro Thr Cys  
100 105



<210> 29  
 <211> 1234  
 <212> DNA  
 <213> Glycine max

<400> 29  
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 ccacaaccca agtcttgatt gttttggaca agcatgagaa cgcgatact tatgtggtag 120  
 ctttccgagg aacggaaccc tttgatgcag atgcatgggt cactgacctt gacatctcat 180  
 ggtacgcatt cccggcattg gaaaaatgca tgggtggcttc atgaaagcct tagggctaca 240  
 gaaaaatgtg ggggtggccta aggagattca aagggatgaa aatcttcccc cgttggccta 300  
 ctatgttatt agggacattc taaggaaagg tttgagtga aatcctaattg caaagtttat 360  
 cattacgggt catagtttgg gtggagcact cgcaatcttg taccctacga tcatgttctt 420  
 gcatgatgag aagttgctga ttgagagggt ggaagggatc tacacgtttg ggcaaccaag 480  
 agttggagat gaagcatatg cacagtatat gagacaaaaa ttgagggaaa attctatcag 540  
 gtattgcagg tttgtttatt gcaatgacat agttccgagg ttgccctatg atgataagga 600  
 cttgctcttc aagcactttg ggatctgcct tttctttaac aggcgctatg aactcaggat 660  
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 caatgctgtt ttggaactaa taaggagctt taccatagcg tacaaaaatg gacctcacta 780  
 tagagaagga tggtttctct ttagtttcag gttggttgg ctgctgattc ctggcttacc 840  
 tgctcacggg ccacaagatt atattaattc cactcttctg ggatcaattg aaaaacattt 900  
 taaagcagat tgatgtgtcc gtatacatga tcattccata ccactacgta catgtgtatg 960  
 gtcatgcaga ctaaaattta cataatcaag atttttagtt ttagaaaaaa tggttaataac 1020  
 acttgattat gtatcatgtg aagaatagtt atgtatcata atgatcatga ataataaac 1080  
 agtttgctgt cagtacgagt tattgtatag taattaataa gctagggtta aagttgtttc 1140  
 ctttggtgca tggatttatc attaatgaga tcaatgtgaa gtttgtttat ttcaaaaaaa 1200  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> 30  
 <211> 246  
 <212> PRT  
 <213> Glycine max

<400> 30  
 His Leu Met Val Arg Ile Pro Gly Ile Gly Lys Met His Gly Gly Phe  
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 Met Lys Ala Leu Gly Leu Gln Lys Asn Val Gly Trp Pro Lys Glu Ile  
 20 25 30  
 Gln Arg Asp Glu Asn Leu Pro Pro Leu Ala Tyr Tyr Val Ile Arg Asp  
 35 40 45  
 Ile Leu Arg Lys Gly Leu Ser Glu Asn Pro Asn Ala Lys Phe Ile Ile  
 50 55 60  
 Thr Gly His Ser Leu Gly Gly Ala Leu Ala Ile Leu Tyr Pro Thr Ile  
 65 70 75 80  
 Met Phe Leu His Asp Glu Lys Leu Leu Ile Glu Arg Leu Glu Gly Ile  
 85 90 95  
 Tyr Thr Phe Gly Gln Pro Arg Val Gly Asp Glu Ala Tyr Ala Gln Tyr  
 100 105 110  
 Met Arg Gln Lys Leu Arg Glu Asn Ser Ile Arg Tyr Cys Arg Phe Val  
 115 120 125  
 Tyr Cys Asn Asp Ile Val Pro Arg Leu Pro Tyr Asp Asp Lys Asp Leu  
 130 135 140



Leu Phe Lys His Phe Gly Ile Cys Leu Phe Phe Asn Arg Arg Tyr Glu  
 145 150 155 160

Leu Arg Ile Leu Glu Glu Glu Pro Asn Lys Asn Tyr Phe Ser Pro Trp  
 165 170 175

Cys Val Ile Pro Met Met Phe Asn Ala Val Leu Glu Leu Ile Arg Ser  
 180 185 190

Phe Thr Ile Ala Tyr Lys Asn Gly Pro His Tyr Arg Glu Gly Trp Phe  
 195 200 205

Leu Phe Ser Phe Arg Leu Val Gly Leu Leu Ile Pro Gly Leu Pro Ala  
 210 215 220

His Gly Pro Gln Asp Tyr Ile Asn Ser Thr Leu Leu Gly Ser Ile Glu  
 225 230 235 240

Lys His Phe Lys Ala Asp  
 245

<210> 31  
 <211> 490  
 <212> DNA  
 <213> Glycine max

<400> 31  
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 ctccataagg gatttgctaa agaagtgttt gaatagaaat gataaagcaa agtttattct 120  
 tacgggtcat agtcttggtg gagcacttgc aattcttttt cccgctatgc taattttgca 180  
 tgctgagaca tttcttttgg aaaggcttga aggggtgtac acatttggac agcctagggt 240  
 tggagatgaa acatttgcta aatacatgga aaatcaattg aaacattatg gcattaagta 300  
 ttttaggttt gtttactgca acgatattgt tcctagggtg ccctttgatg aagatatcat 360  
 gaaatttgag cattttggga catgtcttta ttatgacagg agctatacat gcaaggtaca 420  
 tatataagta ttttaatttt ttgattcatg catatatctg tcattgtaat caactttttt 480  
 ttttctgggg 490

<210> 32  
 <211> 141  
 <212> PRT  
 <213> Glycine max

<400> 32  
 His Glu Glu Arg Trp Pro Lys Glu Ile Glu Thr Asp Glu Asn Arg Pro  
 1 5 10 15

Arg Val Tyr Tyr Ser Ile Arg Asp Leu Leu Lys Lys Cys Leu Asn Arg  
 20 25 30

Asn Asp Lys Ala Lys Phe Ile Leu Thr Gly His Ser Leu Gly Gly Ala  
 35 40 45

Leu Ala Ile Leu Phe Pro Ala Met Leu Ile Leu His Ala Glu Thr Phe  
 50 55 60

Leu Leu Glu Arg Leu Glu Gly Val Tyr Thr Phe Gly Gln Pro Arg Val  
 65 70 75 80

Gly Asp Glu Thr Phe Ala Lys Tyr Met Glu Asn Gln Leu Lys His Tyr  
 85 90 95



Gly	Ile	Lys	Tyr	Phe	Arg	Phe	Val	Tyr	Cys	Asn	Asp	Ile	Val	Pro	Arg
			100					105					110		
Leu	Pro	Phe	Asp	Glu	Asp	Ile	Met	Lys	Phe	Glu	His	Phe	Gly	Thr	Cys
		115					120					125			
Leu	Tyr	Tyr	Asp	Arg	Ser	Tyr	Thr	Cys	Lys	Val	His	Ile			
	130					135					140				

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<210> 33
<211> 774
<212> DNA
<213> Triticum aestivum
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<210> 34
<211> 126
<212> PRT
<213> Triticum aestivum
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$\langle 210 \rangle$	35
$\langle 211 \rangle$	398



<212> PRT  
 <213> Canis familiaris

<400> 35

Met	Trp	Leu	Leu	Leu	Thr	Ala	Ala	Ser	Val	Ile	Ser	Thr	Leu	Gly	Thr	1	5	10	15
Thr	His	Gly	Leu	Phe	Gly	Lys	Leu	His	Pro	Thr	Asn	Pro	Glu	Val	Thr	20	25	30	
Met	Asn	Ile	Ser	Gln	Met	Ile	Thr	Tyr	Trp	Gly	Tyr	Pro	Ala	Glu	Glu	35	40	45	
Tyr	Glu	Val	Val	Thr	Glu	Asp	Gly	Tyr	Ile	Leu	Gly	Ile	Asp	Arg	Ile	50	55	60	
Pro	Tyr	Gly	Arg	Lys	Asn	Ser	Glu	Asn	Ile	Gly	Arg	Arg	Pro	Val	Ala	65	70	75	80
Phe	Leu	Gln	His	Gly	Leu	Leu	Ala	Ser	Ala	Thr	Asn	Trp	Ile	Ser	Asn	85	90	95	
Leu	Pro	Asn	Asn	Ser	Leu	Ala	Phe	Ile	Leu	Ala	Asp	Ala	Gly	Tyr	Asp	100	105	110	
Val	Trp	Leu	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp	Ala	Arg	Arg	Asn	Leu	115	120	125	
Tyr	Tyr	Ser	Pro	Asp	Ser	Val	Glu	Phe	Trp	Ala	Phe	Ser	Phe	Asp	Glu	130	135	140	
Met	Ala	Lys	Tyr	Asp	Leu	Pro	Ala	Thr	Ile	Asp	Phe	Ile	Leu	Lys	Lys	145	150	155	160
Thr	Gly	Gln	Asp	Lys	Leu	His	Tyr	Val	Gly	His	Ser	Gln	Gly	Thr	Thr	165	170	175	
Ile	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Asn	Pro	Lys	Leu	Ala	Lys	Arg	Ile	180	185	190	
Lys	Thr	Phe	Tyr	Ala	Leu	Ala	Pro	Val	Ala	Thr	Val	Lys	Tyr	Thr	Glu	195	200	205	
Thr	Leu	Leu	Asn	Lys	Leu	Met	Leu	Val	Pro	Ser	Phe	Leu	Phe	Lys	Leu	210	215	220	
Ile	Phe	Gly	Asn	Lys	Ile	Phe	Tyr	Pro	His	His	Phe	Phe	Asp	Gln	Phe	225	230	235	240
Leu	Ala	Thr	Glu	Val	Cys	Ser	Arg	Glu	Thr	Val	Asp	Leu	Leu	Cys	Ser	245	250	255	
Asn	Ala	Leu	Phe	Ile	Ile	Cys	Gly	Phe	Asp	Thr	Met	Asn	Leu	Asn	Met	260	265	270	
Ser	Arg	Leu	Asp	Val	Tyr	Leu	Ser	His	Asn	Pro	Ala	Gly	Thr	Ser	Val	275	280	285	
Gln	Asn	Val	Leu	His	Trp	Ser	Gln	Ala	Val	Lys	Ser	Gly	Lys	Phe	Gln	290	295	300	







Ala Leu Ala Pro Ile Gly Ser Val Lys His Ile Lys Gly Phe Leu Ser  
 195 200 205  
 Phe Phe Ala Asn Tyr Phe Ser Leu Glu Phe Asp Gly Trp Phe Asp Ile  
 210 215 220  
 Phe Gly Ala Gly Glu Phe Leu Pro Asn Asn Trp Ala Met Lys Leu Ala  
 225 230 235 240  
 Ala Lys Asp Ile Cys Gly Gly Leu Lys Val Glu Ala Asp Leu Cys Asp  
 245 250 255  
 Asn Val Leu Phe Leu Ile Ala Gly Pro Glu Ser Asp Gln Trp Asn Gln  
 260 265 270  
 Thr Arg Val Pro Val Tyr Ala Thr His Asp Pro Ala Gly Thr Ser Thr  
 275 280 285  
 Gln Asn Ile Val His Trp Met Gln Met Val His His Gly Gly Val Pro  
 290 295 300  
 Ala Tyr Asp Trp Gly Thr Lys Thr Asn Lys Lys Lys Tyr Gly Gln Ala  
 305 310 315 320  
 Asn Pro Pro Glu Tyr Asp Phe Thr Ala Ile Lys Gly Thr Lys Ile Tyr  
 325 330 335  
 Leu Tyr Trp Ser Asp Ala Asp Trp Leu Ala Asp Thr Pro Asp Val Pro  
 340 345 350  
 Asp Tyr Leu Leu Thr Arg Leu Asn Pro Ala Ile Val Ala Gln Asn Asn  
 355 360 365  
 His Leu Pro Asp Tyr Asn His Leu Asp Phe Thr Trp Gly Leu Arg Ala  
 370 375 380  
 Pro Asp Asp Ile Tyr Arg Pro Ala Ile Lys Leu Cys Thr Asp Asp Tyr  
 385 390 395 400  
 Leu Gly Lys